SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Russell, John
          Colpitts, Tracey

(ii) TITLE OF THE INVENTION: REAGENTS AND METHODS USEFUL
          FOR DETECTING DISEASES OF THE PROSTATE

(iii) NUMBER OF SEQUENCES: 16

(iv) CORRESPONDENCE ADDRESS:
   (A) ADDRESSEE: Abbott Laboratories
   (B) STREET: 100 Abbott Park Road
   (C) CITY: Abbott Park
   (D) STATE: IL
   (E) COUNTRY: USA
   (F) ZIP: 60064-3500

(v) COMPUTER READABLE FORM:
   (A) MEDIUM TYPE: Diskette
   (B) COMPUTER: IBM Compatible
   (C) OPERATING SYSTEM: DOS
   (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:
   (A) APPLICATION NUMBER:
   (B) FILING DATE:
   (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
   (A) APPLICATION NUMBER:
   (B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:
   (A) NAME: Becker, Cheryl L.
   (B) REGISTRATION NUMBER: 35,441
   (C) REFERENCE/DOCKET NUMBER: 6105.US.01

(ix) TELECOMMUNICATION INFORMATION:
   (A) TELEPHONE: 847/937-6100
   (B) TELEFAX: 847/938-2623
   (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 279 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
CAGTGACCAT GAAGGCTGTG CTGCTTGCCC TGTTGATGGC AGGCTTGGCC CTGCAGCCAG      60
GCACTGCCCT GCTGTGCTAC TCCTGCAAAG CCCAGGTGAG CAACGAGGAC TGCCTGCAGG     120
TGGAGAACTG CACCCAGCTG GGGGAGCAGT GCTGGACCGC GCGCATCCGC GCAGTTGGCC     180
```

```
TCCTGACCGT CATCAGCAAA GGCTGCAGCT TGAACTGCGT GGATGACTCA CAGGACTACT    240
ACGTGGGCAA GAAGAACATC ACGTGCTGTG ACACCGACT                           279
```

        (2) INFORMATION FOR SEQ ID NO:2:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 207 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
GTGACCATGA AGGCTGTGCT GCTTGCCCTG TTGATGGCAG GCTTGGCCCT GCAGCCAGGC     60
ACTGCCCTGC TGTGCTACTC CTGCAAAGCC CAGGTGAGCA ACGAGGACTG CCTGCAGGTG    120
GAGAACTGCA CCCAGCTGGG GGAGCAGTGC TGGACCGCGC GCATCCGCGC AGTTGGCCTC    180
CTGACCGTCA TCAGCAAAGG CTGCAGC                                        207
```

        (2) INFORMATION FOR SEQ ID NO:3:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 265 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
CGAGGACTGC CTGCAGGTGG AGAACTGCAC CCAGCTGGGG GAGCAGTGCT GGACCGCGCG     60
CATCCGCGCA GTTGGCCTCC TGACCGTCAT CAGCAAAGGC TGCAGCTTGA ACTGCGTGGA    120
TGACTCACAG GACTACTACG TGGGCAAGAA GAACATCACG TGCTGTGACA CCGACTTGTG    180
CAACGCCAGC GGGGCCCATG CCCTGCAGCC GGCTGCCGCC ATCCTTGCGC TGCTCCCTGC    240
ACTCGGCCTG CTGCTCTGGG GACCC                                         265
```

        (2) INFORMATION FOR SEQ ID NO:4:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 196 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
CTCGGCCTGC TGCTCTGGGG ACCCGGCCAG CTATAGGCTC TGGGGGGCCC CGCTGCAGCC     60
CACACTGGGT GTGGTGCCCC AGGCCTCTGT GCCACTCCTC ACAGACCTGG CCCAGTGGGA    120
GCCTGTCCTG GTTCCTGAGG CACATCCTAA CGCAAGTCTG ACCATGTATG TCTGCACCCC    180
TGTNCCCCAC CCTGAC                                                    196
```

        (2) INFORMATION FOR SEQ ID NO:5:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 233 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
CTGGCCCAGT GGGAGCCTGT CCTGGTTCCT GAGGCACATC CTAACGCAAG TCTGACCATG     60
TATGTCTGCN CCCCTGTCCC CCACCCTGAC CCTCCCATGG CCCTCTCCAG GACTCCCACC    120
CGGCAGATCA GCTCTAGTGA CACAGATCCG CCTGCAGATG GCCCCTCCAA CCCTCTCTGC    180
```

TGCTGTTTCC ATGGCCCAGC ATTCTCCACC CTTAACCCTG TGCTCAGGCA CCT   233

    (2) INFORMATION FOR SEQ ID NO:6:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 236 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCCAGCATTC TCCACCCTTA ACCCTGTGCT CAGGCACCTC TTCCCCCAGG AAGCCTTCCC   60
TGCCCACCCC ATCTATGACT TGAGCCAGGT CTGGTCCGTG GTGTCCCCCG CACCCAGCAG   120
GGGACAGGCA CTCAGGAGGG CCCAGTAAAG GCTGAGATGA AGTGGACTGA GTAGAACTGG   180
AGGACAAGAG TCGACGTGAG TTCCTGGGAG TCTCCAGAGA TGGGGCCTGG AGGCCT   236

    (2) INFORMATION FOR SEQ ID NO:7:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 122 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCTGGGAGTC TCCAGAGATG GGGCCTGGAG GCCTGGAGGA ANGGNANCAG GCCTCACATT   60
CGTGGGGCTC CCTGAATGGC AGCCTGAGCA CAGCGTAGGC CCTTAATAAA CACCTGTTGG   120
AT   122

    (2) INFORMATION FOR SEQ ID NO:8:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 968 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CAGTGACCAT GAAGGCTGTG CTGCTTGCCC TGTTGATGGC AGGCTTGGCC CTGCAGCCAG   60
GCACTGCCCT GCTGTGCTAC TCCTGCAAAG CCCAGGTGAG CAACGAGGAC TGCCTGCAGG   120
TGGAGAACTG CACCCAGCTG GGGGAGCAGT GCTGGACCGC GCGCATCCGC GCAGTTGGCC   180
TCCTGACCGT CATCAGCAAA GGCTGCAGCT TGAACTGCGT GGATGACTCA CAGGACTACT   240
ACGTGGGCAA GAAGAACATC ACGTGCTGTG ACACCGACTT GTGCAACGCC AGCGGGGCCC   300
ATGCCCTGCA GCCGGCTGCC GCCATCCTTG CGCTGCTCCC TGCACTCGGC CTGCTGCTCT   360
GGGGACCCGG CCAGCTATAG GCTCTGGGGG GCCCCGCTGC AGCCCACACT GGGTGTGGTG   420
CCCCAGGCCT CTGTGCCACT CCTCACAGAC CTGGCCCAGT GGGAGCCTGT CCTGGTTCCT   480
GAGGCACATC CTAACGCAAG TCTGACCATG TATGTCTGCA CCCCTGTCCC CACCCTGAC   540
CCTCCCATGG CCCTCTCCAG GACTCCCACC CGGCAGATCA GCTCTAGTGA CACAGATCCG   600
CCTGCAGATG GCCCCTCCAA CCCTCTCTGC TGCTGTTTCC ATGGCCCAGC ATTCTCCACC   660
CTTAACCCTG TGCTCAGGCA CCTCTTCCCC CAGGAAGCCT TCCCTGCCCA CCCCATCTAT   720
GACTTGAGCC AGGTCTGGTC CGTGGTGTCC CCGCACCCA GCAGGGGACA GGCACTCAGG   780
AGGGCCCAGT AAAGGCTGAG ATGAAGTGGA CTGAGTAGAA CTGGAGGACA AGAGTCGACG   840
TGAGTTCCTG GGAGTCTCCA GAGATGGGGC CTGGAGGCCT GGAGGAANGG NANCAGGCCT   900
CACATTCGTG GGGCTCCCTG AATGGCAGCC TGAGCACAGC GTAGGCCCTT AATAAACACC   960
TGTTGGAT   968

    (2) INFORMATION FOR SEQ ID NO:9:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 68 base pairs

```
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AGCTCGGAAT TCCGAGCTTG GATCCTCTAG AGCGGCCGCC GACTAGTGAG CTCGTCGACC    60
CGGGAATT                                                            68

        (2) INFORMATION FOR SEQ ID NO:10:

        (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 68 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AATTAATTCC CGGGTCGACG AGCTCACTAG TCGGCGGCCG CTCTAGAGGA TCCAAGCTCG    60
GAATTCCG                                                            68

        (2) INFORMATION FOR SEQ ID NO:11:

        (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 123 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: None

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Lys Ala Val Leu Leu Ala Leu Leu Met Ala Gly Leu Ala Leu Gln
1                   5                   10                  15
Pro Gly Thr Ala Leu Leu Cys Tyr Ser Cys Lys Ala Gln Val Ser Asn
            20                  25                  30
Glu Asp Cys Leu Gln Val Glu Asn Cys Thr Gln Leu Gly Glu Gln Cys
        35                  40                  45
Trp Thr Ala Arg Ile Arg Ala Val Gly Leu Leu Thr Val Ile Ser Lys
        50                  55                  60
Gly Cys Ser Leu Asn Cys Val Asp Asp Ser Gln Asp Tyr Tyr Val Gly
65                  70                  75                  80
Lys Lys Asn Ile Thr Cys Cys Asp Thr Asp Leu Cys Asn Ala Ser Gly
                85                  90                  95
Ala His Ala Leu Gln Pro Ala Ala Ala Ile Leu Ala Leu Leu Pro Ala
            100                 105                 110
Leu Gly Leu Leu Leu Trp Gly Pro Gly Gln Leu
            115                 120

        (2) INFORMATION FOR SEQ ID NO:12:

        (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 34 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: None

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Thr Ala Leu Leu Cys Tyr Ser Cys Lys Ala Gln Val Ser Asn Glu Asp
1                   5                   10                  15
```

```
Cys Leu Gln Val Glu Asn Cys Thr Gln Leu Gly Glu Gln Cys Trp Thr
            20                  25                  30
Ala Arg
```

        (2) INFORMATION FOR SEQ ID NO:13:

        (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 41 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: None

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```
Arg Ile Arg Ala Val Gly Leu Leu Thr Val Ile Ser Lys Gly Cys Ser
1               5                   10                  15
Leu Asn Cys Val Asp Asp Ser Gln Asp Tyr Tyr Val Gly Lys Lys Asn
            20                  25                  30
Ile Thr Cys Cys Asp Thr Asp Leu Cys
        35                  40
```

        (2) INFORMATION FOR SEQ ID NO:14:

        (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 30 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: None

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
Cys Val Asp Asp Ser Gln Asp Tyr Tyr Val Gly Lys Lys Asn Ile Thr
1               5                   10                  15
Cys Cys Asp Thr Asp Leu Cys Asn Ala Ser Gly Ala His Ala
            20                  25                  30
```

        (2) INFORMATION FOR SEQ ID NO:15:

        (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 23 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: None

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```
Leu Gln Pro Ala Ala Ala Ile Leu Ala Leu Leu Pro Ala Leu Gly Leu
1               5                   10                  15
Leu Trp Gly Pro Gly Gln Leu
            20
```

        (2) INFORMATION FOR SEQ ID NO:16:

        (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 8 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Asp Tyr Lys Asp Asp Asp Asp Lys
 1   5